

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH

<120> NUCLEOTIDE SEQUENCES THAT ENCODE CORYNEFORM BACTERIA FOR PROTEINS PARTICIPATING IN THE BIOSYNTHESIS OF L-SERINE AND METHOD OF PRODUCING L-SERINE

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<170> PatentIn Ver. 2.1

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<213> Corynebacterium glutamicum

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Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
50 55 60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
65 70 75 80

Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
85 90 95

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
100 105 110

Leu Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg
115 120 125

Glu Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly
130 135 140

Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
145 150 155 160

Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
165 170 175

Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
180 185 190

Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
195 200 205

Thr Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser
210 215 220

Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
225 230 235 240

Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
 180 185 190
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
 195 200 205
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser
 210 215 220
 Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp
 225 230 235 240
 Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala
 245 250 255
 Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe
 260 265 270
 Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu
 275 280 285
 Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys
 290 295 300
 Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly Gly
 305 310 315 320
 Arg Val Gly Glu Glu
 325

<210> 11
 <211> 319
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 11
 Met Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
 1 5 10 15
 Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val
 20 25 30
 Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
 35 40 45
 Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala
 50 55 60
 Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp
 65 70 75 80
 Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn
 85 90 95
 Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu
 100 105 110
 Leu Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg
 115 120 125

Ala	Pro	Thr	Ser	Asn	Ile	His	Ser	Ala	Cys	Glu	His	Ala	Ile	Ser	Leu	100	105	110
Leu	Leu	Ser	Thr	Ala	Arg	Gln	Ile	Pro	Ala	Ala	Asp	Ala	Thr	Leu	Arg	115	120	125
Glu	Gly	Glu	Trp	Lys	Arg	Ser	Ser	Phe	Asn	Gly	Val	Glu	Ile	Phe	Gly	130	135	140
Lys	Thr	Val	Gly	Ile	Val	Gly	Phe	Gly	His	Ile	Gly	Gln	Leu	Phe	Ala	145	150	155
Gln	Arg	Leu	Ala	Ala	Phe	Glu	Thr	Thr	Ile	Val	Ala	Tyr	Asp	Pro	Tyr	165	170	175
Ala	Asn	Pro	Ala	Arg	Ala	Ala	Gln	Leu	Asn	Val	Glu	Leu	Val	Glu	Leu	180	185	190
Asp	Glu	Leu	Met	Ser	Arg	Ser	Asp	Phe	Val	Thr	Ile	His	Leu	Pro	Lys	195	200	205
Thr	Lys	Glu	Thr	Ala	Gly	Met	Phe	Asp	Ala	Gln	Leu	Leu	Ala	Lys	Ser	210	215	220
Lys	Lys	Gly	Gln	Ile	Ile	Ile	Asn	Ala	Ala	Arg	Gly	Gly	Leu	Val	Asp	225	230	235
Glu	Gln	Ala	Leu	Ala	Asp	Ala	Ile	Glu	Ser	Gly	His	Ile	Arg	Gly	Ala	245	250	255
Gly	Phe	Asp	Val	Tyr	Ser	Thr	Glu	Pro	Cys	Thr	Asp	Ser	Pro	Leu	Phe	260	265	270
Lys	Leu	Pro	Gln	Val	Val	Val	Thr	Pro	His	Leu	Gly	Ala	Ser	Thr	Glu	275	280	285
Glu	Ala	Gln	Asp	Arg	Ala	Gly	Thr	Asp	Val	Ala	Asp	Ser	Val	Leu	Lys	290	295	300
Ala	Leu	Ala	Gly	Glu	Phe	Val	Ala	Asp	Ala	Val	Asn	Val	Ser	Gly	Gly	305	310	315
Arg	Val	Gly	Glu	Glu	Val	Ala	Val	Trp	Met	Asp	Leu	Ala	Arg	Lys	Leu	325	330	335
Gly	Leu	Leu	Ala	Gly	Lys	Leu	Val	Asp	Ala	Ala	Pro	Val	Ser	Ile	Glu	340	345	350
Val	Glu	Ala	Arg	Gly	Glu	Leu	Ser	Ser	Glu	Gln	Val	Asp	Ala	Leu	Gly	355	360	365
Leu	Ser	Ala	Val	Arg	Gly	Leu	Phe	Ser	Gly	Ile	Ile	Glu	Glu	Ser	Val	370	375	380
Thr	Phe	Val	Asn	Ala	Pro	Arg	Ile	Ala	Glu	Glu	Arg	Gly	Leu	Asp	Ile	385	390	395
Ser	Val	Lys	Thr	Asn	Ser	Glu	Ser	Val	Thr	His	Arg	Ser	Val	Leu	Gln	405	410	415

Val Lys Val Ile Thr Gly Ser Gly Ala Ser Ala Thr Val Val Gly Ala
 420 425 430
 Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile Asn Gly Arg
 435 440 445
 Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu Gln Tyr Thr
 450 455 460
 Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu Gly Ala Ala
 465 470 475 480
 Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu Lys Gly Asp
 485 490 495
 Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser Glu Glu Leu
 500 505 510
 Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe Gln Val Asp
 515 520 525
 Leu Asp
 530

<210> 13
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic Construct
 <400> 13

tctagagccg gagacgtgaa taaaat

26

<210> 14
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic Construct
 <400> 14

ggatccgact ggtgagggtc aagtcc

26

<210> 15
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic Construct

<400> 15

ggatccttaa ccggaacgt tcacagc

27

<210> 16

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 16

ggatccttac tcttcgccca cgcgacc

27

<210> 17

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 17

ggatacctta agccagaatc catccacaca g

31

<210> 18

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 18

ggatccttac ttgccagcaa gaaaagacc

29

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

<400> 19

ggatccttaa tccaggccac ggccatt

27